



1/19

SEQUENCE LISTING

<110> Segre, Gino V.
Kronenberg, Henry M.
Abou-Samra, Abdul-Badi
Juppner, Harald
Potts, Jr., John T.
Schipani, Ernestina

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tcg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc	163
Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val	
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Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile	
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Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu	
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gtc ctc agg gtc cct gaa ctt gct gaa tct gcc aaa gac tgg atg tca	307
Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser	
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agg tct gca aag aca aag aag gag aaa cct gca gaa aag ctt tat ccc	355
Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro	
75 80 85	

cag gca gag gag tcc agg gaa gtt tct gac agg agc cgg ctg cag gat	403
Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp	
90 95 100	

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ctc act gtg gct gtg ctg att ctg ggt tac ttt agg agg tta cat tgc Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys 200 205 210	739
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 Val Pro Ile Leu Ala Ala Ile Val Val Asn Phe Ile Leu Phe Ile Asn
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 Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg
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 Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val
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 Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro
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 Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln Val Gln Met His Tyr Glu
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 Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg
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 Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser
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 Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val
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Met Gly Ala Pro Arg Ile	
1 5	
tcg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc	163
Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val	
10 15 20	
tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc	211
Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile	
25 30 35	
att ctt ctg cgc aat gcc cag gcc cag tgt gag cag cgc ctg aaa gag	259
Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu	
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gtc ctc agg gtc cct gaa ctt gct gaa tct gcc aaa gac tgg atg tca	307
Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser	
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Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro	
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Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly	
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Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp	
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Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser	
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Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu	
155 160 165	
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Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp	
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cgc ctc gga atg atc tac act gtg ggc tac tcc atc tct ctg ggc tcc	691
Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser	
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ctc act gtg gct gtg ctg att ctg ggt tac ttt agg agg tta cat tgc	739
Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys	
200 205 210	
acc cga aac tac att cac atg cat ctc ttc gtg tcc ttt atg ctc cgg	787
Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg	
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Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val
490 495 500

gga cct cga ggg ggg ctg gcc ttg tcc ctc agc cct cga cta gct cct 1651
Gly Pro Arg Gly Gly Leu Ala Leu Ser Leu Ser Pro Arg Leu Ala Pro
505 510 515

ggg gct gga gcc agt gcc aat ggc cat cac cag ttg cct ggc tat gtg 1699
Gly Ala Gly Ala Ser Ala Asn Gly His His Gln Leu Pro Gly Tyr Val
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aag cat ggt tcc att tct gag aac tca ttg cct tca tct ggc cca gag 1747
Lys His Gly Ser Ile Ser Glu Asn Ser Leu Pro Ser Ser Gly Pro Glu
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cct ggc acc aaa gat gac ggg tat ctc aat ggc tct gga ctt tat gag 1795
Pro Gly Thr Lys Asp Asp Gly Tyr Leu Asn Gly Ser Gly Leu Tyr Glu
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Asp Val Phe Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln
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gcg caa tgt gac aag ctg ctc aag gaa gtt ctg cac aca gca gcc aac 255
Ala Gln Cys Asp Lys Leu Leu Lys Glu Val Leu His Thr Ala Ala Asn
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ccc agg aaa gag aag gca tgc gga aag ttc tac cct gag tct aaa gag Pro Arg Lys Glu Lys Ala Ser Gly Lys Phe Tyr Pro Glu Ser Lys Glu 80 85 90	351
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APR 18 2000

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gtc atg tgactgggca ctagggggct agactgctgg cctgggcaca tggacagatg Val Met 590	1895
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cgc ccc tgt ctg ccg gaa tgg gac cac atc ctg tgc tgg ccg ctg ggg Arg Pro Cys Leu Pro Glu Trp Asp His Ile Leu Cys Trp Pro Leu Gly 110 115 120	390

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gcc gtg agc atc ttc gtc aag gac gct gtg ctc tac tct ggc gcc acg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr 235 240 245	774
ctt gat gag gct gag cgc ctc acc gag gag gag ctg cgc gcc atc gcc Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala 250 255 260 265	822
cag gcg ccc ccg ccg cct gcc acc gcc gct gcc ggc tac gcg ggc tgc Gln Ala Pro Pro Pro Pro Ala Thr Ala Ala Gly Tyr Ala Gly Cys 270 275 280	870
agg gtg gct gtg acc ttc ttc ctt tac ttc ctg gcc acc aac tac tac Arg Val Ala Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr 285 290 295	918
tgg att ctg gtg gag ggg ctg tac ctg cac agc ctc atc ttc atg gcc Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala 300 305 310	966
ttc ttc tca gag aag aag tac ctg tgg ggc ttc aca gtc ttc ggc tgg Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp 315 320 325	1014
ggt ctg ccc gct gtc ttc gtg gct gtg tgg gtc agt gtc aga gct acc Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Ser Val Arg Ala Thr 330 335 340 345	1062
ctg gcc aac acc ggg tgc tgg gac ttg agc tcc ggg aac aaa aag tgg Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp 350 355 360	1110

atc atc cag gtg ccc atc ctg gcc tcc att gtg ctc aac ttc atc ctc Ile Ile Gln Val Pro Ile Leu Ala Ser Ile Val Leu Asn Phe Ile Leu 365 370 375	1158
ttc atc aat atc gtc cgg gtg ctc gcc acc aag cag cgg gag acc aac Phe Ile Asn Ile Val Arg Val Leu Ala Thr Lys Gln Arg Glu Thr Asn 380 385 390	1206
gcc ggc cgg tgt gac aca cgg cag cag tac cgg aag ctg ctc aaa tcc Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser 395 400 405	1254
acg ctg gtg ctc atg ccc ctc ttt ggc gtc cac tac att gtc ttc atg Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met 410 415 420 425	1302
gcc aca cca tac acc gag gtc tca ggg acg ctc tgg caa gtc cag atg Ala Thr Pro Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Val Gln Met 430 435 440	1350
cac tat gag atg ctc ttc aac tcc ttc cag gga ttt ttt gtc gca atc His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile 445 450 455	1398
ata tac tgt ttc tgc aat ggc gag gta caa gct gag atc aag aaa tct Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser 460 465 470	1446
tgg agc cgc tgg aca ctg gca ctg gac ttc aag cga aag gca cgc agc Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser 475 480 485	1494
ggg agc agc agc tat agc tac ggc ccc atg gtg tcc cac aca agt gtg Gly Ser Ser Ser Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val 490 495 500 505	1542
acc aat gtc ggc ccc cgt gtg gga ctc ggc ctg ccc ctc agc ccc cgc Thr Asn Val Gly Pro Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg 510 515 520	1590
cta ctg ccc act gcc acc acc aac ggc cac cct cag ctg cct ggc cat Leu Leu Pro Thr Ala Thr Thr Asn Gly His Pro Gln Leu Pro Gly His 525 530 535	1638
gcc aag cca ggg acc cca gcc ctg gag acc ctc gag acc aca cca cct Ala Lys Pro Gly Thr Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro 540 545 550	1686
gcc atg gct gct ccc aag gac gat ggg ttc ctc aac ggc tcc tgc tca Ala Met Ala Ala Pro Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser 555 560 565	1734
ggc ctg gac gag gag gcc tct ggg cct gag cgg cca cct gcc ctg cta Gly Leu Asp Glu Glu Ala Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu 570 575 580 585	1782
cag gaa gag tgg gag aca gtc atg tgaccaggcg ctgggggctg gacctgctga Gln Glu Glu Trp Glu Thr Val Met 590	1836
catagtggat ggacagatgg accaaaagat ggggtggttga atgatttccc actcagggcc tgggggccaag aggaaaaaac aggggaaaaa agaaaaaaa aagaaaaaag gaaaaaaa	1896 1956

12/19

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2010

<210> 5
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> binding; 1st to last; peptide fragment

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Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile
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Tyr Thr Val Gly
20

<210> 6
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> binding; 1st to last; peptide fragment

<400> 6
Tyr Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu
1 5 10 15
Glu Glu Leu

<210> 7
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> binding; 1st to last; peptide fragment

<400> 7
Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu
1 5 10 15
Val Glu Gly

<210> 8
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> binding; 1st to last; peptide fragment

<221> VARIANT
<222> (1)...(26)
<223> Xaa = Any Amino Acid

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Tyr Xaa Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser Ser
1 5 10 15
Gly His Lys Lys Trp Ile Ile Gln Val Pro
20 25

<210> 9
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> binding; 1st to last; peptide fragment

<400> 9
 Pro Tyr Thr Glu Tyr Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr
 1 5 10 15
 Glu Met

<210> 10
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> binding; 1st to last; peptide fragment

<400> 10
 Asp Asp Val Phe Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala
 1 5 10 15
 Gln Ala

<210> 11
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> binding; 1st to last; peptide fragment

<400> 11
 Phe Phe Arg Leu His Cys Thr Arg Asn Tyr
 1 5 10

<210> 12
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> binding; 1st to last; peptide fragment

<400> 12
 Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu
 1 5 10

<210> 13
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> binding; 1st to last; peptide fragment

<400> 13
 Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr
 1 5 10 15
 Arg Gln Gln Tyr Arg Lys Leu Leu Lys
 20 25

<210> 14
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1st to last; primer

<400> 14
 agatgaggct gtgcaggt 18

<210> 15
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1st to last; primer

<400> 15
 ggaattccat gggagcggcc cggat 25

<210> 16
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1st to last; primer

<400> 16
 cgggatcccg cggccctagg cggat 24

<210> 17
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1st to last; primer

<400> 17
 agtatagcgt ccttgacga 19

<210> 18
 <211> 515
 <212> PRT
 <213> Didelphoidea

<400> 18
 Met Gly Ala Pro Arg Ile Ser His Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Ser Val Leu Ser Ser Val Tyr Ala Leu Val Asp Ala Asp Asp Val Ile
 20 25 30
 Thr Lys Glu Glu Gln Ile Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys
 35 40 45

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<210> 19
 <211> 585
 <212> PRT
 <213> Didelphoidea

<400> 19
 Met Gly Ala Pro Arg Ile Ser His Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Ser Val Leu Ser Val Tyr Ala Leu Val Asp Ala Asp Asp Val Ile
 20 25 30
 Thr Lys Glu Glu Gln Ile Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys
 35 40 45
 Glu Gln Arg Leu Lys Glu Val Leu Arg Val Pro Glu Leu Ala Glu Ser
 50 55 60
 Ala Lys Asp Trp Met Ser Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro
 65 70 75 80
 Ala Glu Lys Leu Tyr Pro Gln Ala Glu Glu Ser Arg Glu Val Ser Asp
 85 90 95
 Arg Ser Arg Leu Gln Asp Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile
 100 105 110
 Val Cys Trp Pro Ala Gly Val Pro Gly Lys Val Val Ala Val Pro Cys
 115 120 125
 Pro Asp Tyr Phe Tyr Asp Phe Asn His Lys Gly Arg Ala Tyr Arg Arg
 130 135 140
 Cys Asp Ser Asn Gly Ser Trp Glu Leu Val Pro Gly Asn Asn Arg Thr
 145 150 155 160
 Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn Glu Thr Arg
 165 170 175
 Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
 180 185 190
 Ser Ile Ser Leu Gly Ser Leu Thr Val Ala Val Leu Ile Leu Gly Tyr
 195 200 205
 Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe
 210 215 220
 Val Ser Phe Met Leu Arg Ala Val Ser Ile Phe Ile Lys Asp Ala Val
 225 230 235 240
 Leu Tyr Ser Gly Val Ser Thr Asp Glu Ile Glu Arg Ile Thr Glu Glu
 245 250 255
 Glu Leu Arg Ala Phe Thr Glu Pro Pro Ala Asp Lys Ala Gly Phe
 260 265 270
 Val Gly Cys Arg Val Ala Val Thr Val Phe Leu Tyr Phe Leu Thr Thr
 275 280 285
 Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile
 290 295 300
 Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu
 305 310 315 320
 Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Thr Val
 325 330 335
 Arg Ala Thr Leu Ala Asn Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn
 340 345 350
 Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ala Ile Val Val Asn
 355 360 365
 Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr Lys Leu Arg
 370 375 380
 Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu
 385 390 395 400
 Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile
 405 410 415
 Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln
 420 425 430
 Val Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe
 435 440 445

Val	Ala	Ile	Ile	Tyr	Cys	Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Il
450						455					460				
Lys	Lys	Ser	Trp	Ser	Arg	Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys
465					470					475					480
Ala	Arg	Ser	Gly	Ser	Ser	Thr	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His
				485					490					495	
Thr	Ser	Val	Thr	Asn	Val	Gly	Pro	Arg	Gly	Gly	Leu	Ala	Leu	Ser	Leu
			500					505					510		
Ser	Pro	Arg	Leu	Ala	Pro	Gly	Ala	Gly	Ala	Ser	Ala	Asn	Gly	His	His
		515					520					525			
Gln	Leu	Pro	Gly	Tyr	Val	Lys	His	Gly	Ser	Ile	Ser	Glu	Asn	Ser	Leu
	530					535					540				
Pro	Ser	Ser	Gly	Pro	Glu	Pro	Gly	Thr	Lys	Asp	Asp	Gly	Tyr	Leu	Asn
545					550					555					560
Gly	Ser	Gly	Leu	Tyr	Glu	Pro	Met	Val	Gly	Glu	Gln	Pro	Pro	Pro	Leu
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Leu	Glu	Glu	Glu	Arg	Glu	Thr	Val	Met							
			580					585							

<210> 20
 <211> 591
 <212> PRT
 <213> Rattus rattus

<400> 20

Met	Gly	Ala	Ala	Arg	Ile	Ala	Pro	Ser	Leu	Ala	Leu	Leu	Leu	Cys	Cys
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Pro	Val	Leu	Ser	Ser	Ala	Tyr	Ala	Leu	Val	Asp	Ala	Asp	Asp	Val	Phe
			20					25					30		
Thr	Lys	Glu	Glu	Gln	Ile	Phe	Leu	Leu	His	Arg	Ala	Gln	Ala	Gln	Cys
		35					40					45			
Asp	Lys	Leu	Leu	Lys	Glu	Val	Leu	His	Thr	Ala	Ala	Asn	Ile	Met	Glu
	50					55					60				
Ser	Asp	Lys	Gly	Trp	Thr	Pro	Ala	Ser	Thr	Ser	Gly	Lys	Pro	Arg	Lys
	65				70					75					80
Glu	Lys	Ala	Ser	Gly	Lys	Phe	Tyr	Pro	Glu	Ser	Lys	Glu	Asn	Lys	Asp
				85					90					95	
Val	Pro	Thr	Gly	Ser	Arg	Arg	Arg	Gly	Arg	Pro	Cys	Leu	Pro	Glu	Trp
			100					105					110		
Asp	Asn	Ile	Val	Cys	Trp	Pro	Leu	Gly	Ala	Pro	Gly	Glu	Val	Val	Ala
		115					120					125			
Val	Pro	Cys	Pro	Asp	Tyr	Ile	Tyr	Asp	Phe	Asn	His	Lys	Gly	His	Ala
	130					135					140				
Tyr	Arg	Arg	Cys	Asp	Arg	Asn	Gly	Ser	Trp	Glu	Val	Val	Pro	Gly	His
	145				150					155					160
Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	Cys	Leu	Lys	Phe	Met	Thr	Asn
				165					170					175	
Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	Arg	Leu	Gly	Met	Ile	Tyr	Thr
			180					185					190		
Val	Gly	Tyr	Ser	Met	Ser	Leu	Ala	Ser	Leu	Thr	Val	Ala	Val	Leu	Ile
		195					200					205			
Leu	Ala	Tyr	Phe	Arg	Arg	Leu	His	Cys	Thr	Arg	Asn	Tyr	Ile	His	Met
	210					215					220				
His	Met	Phe	Leu	Ser	Phe	Met	Leu	Arg	Ala	Ala	Ser	Ile	Phe	Val	Lys
	225				230					235					240
Asp	Ala	Val	Leu	Tyr	Ser	Gly	Phe	Thr	Leu	Asp	Glu	Ala	Glu	Arg	Leu
				245					250					255	
Thr	Glu	Glu	Glu	Leu	His	Ile	Ile	Ala	Gln	Val	Pro	Pro	Pro	Pro	Ala
			260					265					270		
Ala	Ala	Ala	Val	Gly	Tyr	Ala	Gly	Cys	Arg	Val	Ala	Val	Thr	Phe	Phe
			275				280						285		

Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu
 290 295 300
 Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr
 305 310 315 320
 Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val
 325 330 335
 Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp
 340 345 350
 Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
 355 360 365
 Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val
 370 375 380
 Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg
 385 390 395 400
 Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu
 405 410 415
 Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val
 420 425 430
 Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn
 435 440 445
 Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly
 450 455 460
 Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala
 465 470 475 480
 Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 485 490 495
 Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala
 500 505 510
 Gly Leu Ser Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn
 515 520 525
 Gly His Ser Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr
 530 535 540
 Glu Thr Glu Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly
 545 550 555 560
 Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser
 565 570 575
 Ala Arg Pro Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr Val Met
 580 585 590

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 <211> 593
 <212> PRT
 <213> Homo sapiens

<400> 21
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 Thr Lys Glu Glu Gln Ile Phe Leu His Arg Ala Gln Ala Gln Cys
 35 40 45
 Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu
 50 55 60
 Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys
 65 70 75 80
 Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu
 85 90 95
 Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp
 100 105 110
 Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala
 115 120 125

[illegible]